

Sequence Listing

<110> Lee, James
Wood, William I.

<120> VEGF-RELATED PROTEIN

<130> P0963R1D1

<140> US 09/313,299

<141> 1999-05-17

<150> US 08/706,054

<151> 1996-08-30

<150> US 60/003,491

<151> 1995-09-08

<160> 12

<210> 1

<211> 2031

<212> DNA

<213> artificial sequence

<400> 1

cgcggggtgt tctggtgtcc cccgccccgc ctctccaaaa agctacaccg 50
acgcggaccg cggcggcgtc ctccctcgcc ctgccttcac ctgcggggct 100
ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggg ttttacctga 150
caccgcgcgc ctttccccgg cactggctgg gagggcgccc tgcaaaagttg 200
ggaacgcgga gccccggacc cgtcccgcc gctccggct cggccagggg 250
gggtcgccgg gaggagcccg ggggagaggg accaggaggg gcccgcggcc 300
tcgcaggggc gccgcgcgc ccacccctgc ccccgccagc ggaccgggtcc 350
cccacccccg gtccttcac catgcacttg ctgggcttct tctctgtggc 400
gtgttctctg ctgcgcgtg cgtgtctccc gggctctcgc gaggcgcccg 450
ccgcgcgcgc cgccttcgag tccggactcg acctctcgga cgcggagccc 500
gacgcggggc aggccacggc ttatgcaagc aaagatctgg aggagcagtt 550
acggtctgtg tccagtgtag atgaactcat gactgtactc taccagaat 600
attggaaaat gtacaagtgt gagctaagga aaggaggctg gcaacataac 650
agagaacagg ccaacctcaa ctcaaggaca gaagagacta taaaatttgc 700
tgcagcacat tataatacag agatcttgaa aagtattgat aatgagtgga 750
gaaagactca atgcatgcca cgggaggtgt gtatagatgt ggggaaggag 800
tttggagtgc cgacaaacac cttctttaa cctccatgtg tgtccgtcta 850
cagatgtggg ggttgctgca atagtgggg gctgcagtgc atgaacacca 900

gcacgagcta cctcagcaag acgttatattg aaattacagt gcctctctct 950
5 caaggcccca aaccagtaac aatcagtttt gccaatcaca cttcctgccg 1000
atgcatgtct aaactggatg tttacagaca agttcattcc attattagac 1050
gttccctgcc agcaacacta ccacagtgtc aggcagcgaa caagacctgc 1100
10 cccaccaatt acatgtggaa taatcacatc tgcagatgcc tggctcagga 1150
agattttatg ttttctcgg atgctggaga tgactcaaca gatggattcc 1200
atgacatctg tggaccaaac aaggagctgg atgaagagac ctgtcagtgt 1250
15 gtctgcagag cggggcttcg gcctgccagc tgtggacccc acaaagaact 1300
agacagaaac tcatgccagt gtgtctgtaa aaacaaactc tccccagcc 1350
20 aatgtggggc caaccgagaa tttgatgaaa acacatgcca gtgtgtatgt 1400
aaaagaacct gccccagaaa tcaaccccta aatcctggaa aatgtgcctg 1450
tgaatgtaca gaaagtccac agaaatgctt gttaaaagga aagaagttcc 1500
25 accacaaac atgcagctgt tacagacggc catgtacgaa ccgccagaag 1550
gcttgtgagc caggattttc atatagttaa gaagtgtgtc gttgtgtccc 1600
30 ttcattattg aaaagaccac aaatgagcta agattgtact gttttccagt 1650
tcatcgattt tctattatgg aaaactgtgt tgccacagta gaactgtctg 1700
tgaacagaga gacccttgtg ggtccatgct aacaaagaca aaagtctgtc 1750
35 tttcctgaac catgtggata actttacaga aatggactgg agctcatctg 1800
caaaaggcct cttgtaaaga ctggttttct gccaatgacc aaacagccaa 1850
40 gattttcctc ttgtgatttc tttaaaagaa tgactatata atttatttcc 1900
actaaaaata ttgtttctgc attcattttt atagcaacaa caattggtaa 1950
aactcactgt gatcaatatt tttatatcat gcaaaatatg tttaaaataa 2000
45 aatgaaaatt gtattaaaaa aaaaaaaaaa a 2031

<210> 2

<211> 2031

50 <212> DNA

<213> artificial sequence

<400> 2

55 tttttttttt ttttttaata caattttcat tttattttta acatattttg 50
catgatataa aaatattgat cacagtgagt tttaccaatt gttgttgcta 100
taaaaatgaa tgcagaacaa atatttttag tggaaataaa ttatatagtc 150
60 attcttttaa agaaatcaca agaggaaaat cttggctgtt tggtcattgg 200

cagaaaacca gtctttacaa gaggcctttt gcagatgagc tccagtccat 250
 ttctgtaaag ttatccacat gggttcaggaa agacagactt ttgtctttgt 300
 5 tagcatggac ccacaagggt ctctctgttc acagacagtt ctactgtggc 350
 aacacagttt tccataatag aaaatcgatg aactggaaaa cagtacaatc 400
 10 ttagctcatt tgtggctctt tccaatatga agggacacaa cgacacactt 450
 cttcactata tgaaaatcct ggctcacaag ccttctggcg gttcgtacat 500
 ggccgtctgt aacagctgca tgtttgggtg tggaacttct ttcttttaa 550
 15 caagcatttc tgtggacttt ctgtacattc acaggcacat tttccaggat 600
 ttaggggttg atttctgggg caggttcttt tacatacaca ctggcatgtg 650
 20 ttttcatcaa attctcggtt ggccccacat tggctgggga agagtgtgtt 700
 tttacagaca cactggcatg agtttctgtc tagttctttg tgggggtccac 750
 agctggcagg ccgaagcccc gctctgcaga cacactgaca ggtctcttca 800
 25 tccagctcct tgtttgggtc acagatgtca tggaatccat ctgttgagtc 850
 atctccagca tccgaggaaa acataaaatc ttcttgagcc aggcactctgc 900
 30 agatgtgatt attccacatg taattgggtg ggcaggtctt gttcgtctgc 950
 tgacactgtg gtagtggtgc tggcagggaa cgtctaataa tggaatgaac 1000
 ttgtctgtaa acatccagtt tagacatgca tcggcaggaa gtgtgattgg 1050
 35 caaaactgat tgttactggg ttggggcctt gagagagagg cactgtaatt 1100
 tcaaataacg tcttgtctgag gtagctcgtg ctgggtgtca tgcactgcag 1150
 40 cccctcacta ttgcagcaac ccccatctct gtagacggac acacatggag 1200
 gtttaaagaa ggtgtttgtc ggcactccaa actcctccc cacatctata 1250
 cacacctccc gtggcatgca ttgagtcctt ctccactcat tatcaatact 1300
 45 tttcaagatc tctgtattat aatgtgctgc agcaaatttt atagtctctt 1350
 ctgtccttga gttgaggttg gcctgttctc tgttatgttg ccagcctcct 1400
 50 ttcttagct gacacttgta ctttttccaa tattctgggt agagtacagt 1450
 catgagttca tctacactgg acacagaccg taactgctcc tccagatctt 1500
 tgcttgcata agccgtggcc tcgcccgcgt cgggctccgc gtccgagagg 1550
 55 tcgagtccgg actcgaaggc ggcggcggcg gcgggcgcct cgcgaggacc 1600
 cgggagcagc acagcggcga gcagagaaca cgccacagag aagaagccca 1650
 60 gcaagtgcac ggtggaagga ccgggggtgg gggaccggtc cgctggcggg 1700
 ggcaggggtg ggggcgcggg cgccctgcg aggccgcggg cccctcctgg 1750

tccctctccc ccgggtcct cccggcgacc cccctgggc gagccggagg 1800
 5 cggcgggagc ggggtccggg ctccgcgttc ccaactttgc agggcgccct 1850
 cccagccagt accggggaaa ggcggcggt gtcaggtaaa agcctcacag 1900
 gaaaccggac atccgagctc cccgcattcg gagcccgca ggtgaagcga 1950
 10 gggcgaggga ggacgccgc gcggtccgcg tcggtgtagc tttttggaga 2000
 ggcggggcgg gggacaccag aacacccgc g 2031

15 <210> 3
 <211> 419
 <212> PRT
 <213> artificial sequence

20 <400> 3
 Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala
 1 5 10 15
 Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala
 20 25 30
 25 Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
 35 40 45
 30 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
 50 55 60
 Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
 65 70 75
 35 Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
 80 85 90
 Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
 95 100 105
 40 Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
 110 115 120
 Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 45 125 130 135
 Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
 140 145 150
 50 Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
 155 160 165
 Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr
 55 170 175 180
 Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly
 185 190 195
 60 Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
 200 205 210

	Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	His	Ser	Ile	Ile	
					215					220					225	
5	Arg	Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	Ala	Ala	Asn	
					230					235					240	
	Lys	Thr	Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	Cys	Arg	
					245					250					255	
10	Cys	Leu	Ala	Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	Asp	
					260					265					270	
	Asp	Ser	Thr	Asp	Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	
					275					280					285	
15	Leu	Asp	Glu	Glu	Thr	Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	
					290					295					300	
	Pro	Ala	Ser	Cys	Gly	Pro	His	Lys	Glu	Leu	Asp	Arg	Asn	Ser	Cys	
20					305					310					315	
	Gln	Cys	Val	Cys	Lys	Asn	Lys	Leu	Phe	Pro	Ser	Gln	Cys	Gly	Ala	
					320					325					330	
25	Asn	Arg	Glu	Phe	Asp	Glu	Asn	Thr	Cys	Gln	Cys	Val	Cys	Lys	Arg	
					335					340					345	
	Thr	Cys	Pro	Arg	Asn	Gln	Pro	Leu	Asn	Pro	Gly	Lys	Cys	Ala	Cys	
					350					355					360	
30	Glu	Cys	Thr	Glu	Ser	Pro	Gln	Lys	Cys	Leu	Leu	Lys	Gly	Lys	Lys	
					365					370					375	
	Phe	His	His	Gln	Thr	Cys	Ser	Cys	Tyr	Arg	Arg	Pro	Cys	Thr	Asn	
35					380					385					390	
	Arg	Gln	Lys	Ala	Cys	Glu	Pro	Gly	Phe	Ser	Tyr	Ser	Glu	Glu	Val	
					395					400					405	
40	Cys	Arg	Cys	Val	Pro	Ser	Tyr	Trp	Lys	Arg	Pro	Gln	Met	Ser		
					410					415				419		
	<210> 4															
	<211> 147															
45	<212> PRT															
	<213> artificial sequence															
	<400> 4															
50	Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	
	1				5					10					15	
	Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	
					20					25					30	
55	Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	
					35					40					45	
	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	
					50					55					60	
60	Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	

	65	70	75
	Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu		
	80	85	90
5	Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln		
	95	100	105
10	Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met		
	110	115	120
	Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp		
	125	130	135
15	Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg		
	140	145	147
	<210> 5		
	<211> 149		
20	<212> PRT		
	<213> artificial sequence		
	<400> 5		
25	Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala		
	1	5	10
	Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser		
	20	25	30
30	Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu		
	35	40	45
	Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp		
	50	55	60
35	Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro		
	65	70	75
40	Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu		
	80	85	90
	Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln		
	95	100	105
45	Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu		
	110	115	120
	Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu		
	125	130	135
50	Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg		
	140	145	149
	<210> 6		
55	<211> 299		
	<212> DNA		
	<213> artificial sequence		
	<220>		
60	<221> unknown		
	<222> 74		

<223> unknown base

<400> 6

ccgtctacag atgtgggggt tgctgcaata gtgaggggct gcagtgcattg 50

aacaccagca cgagctacct cagnaagacg ttatttgaaa ttacagtgcc 100

tctctctcaa ggccccaaac cagtaacaat cagttttgcc aatcacactt 150

cctgccgatg catgtctaaa ctggatgttt acagacaagt tcattccact 200

attagacgtt ccctgccagc aacactacca cagtgtcagg cagcgaacaa 250

gacctgcccc accaattaca tgtggaataa tcacatctgc agatgcctg 299

<210> 7

<211> 50

<212> DNA

<213> artificial sequence

<400> 7

ctggtgttca tgcactgcag cccctcacta ttgcagcaac cccacatct 50

<210> 8

<211> 50

<212> DNA

<213> artificial sequence

<400> 8

gcattctgcag atgtgattat tccacatgta attggtgggg caggtcttgt 50

<210> 9

<211> 8

<212> PRT

<213> artificial sequence

<400> 9

Tyr	Ser	Met	Thr	Pro	Pro	Thr	Leu
1				5			8

<210> 10

<211> 9

<212> PRT

<213> artificial sequence

<400> 10

Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln	Asp
1				5				9

<210> 11

<211> 40

<212> PRT

<213> artificial sequence

<400> 11

Lys	Tyr	Ala	Leu	Ala	Asp	Ala	Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn
1				5					10					15

Arg	Phe	Arg	Gly	Lys	Asp	Leu	Pro	Val	Leu	Asp	Gln	Leu	Leu	Glu
				20					25					30

Gly Gly Ala Ala His Tyr Ala Leu Leu Pro
35 40

5 <210> 12
<211> 13
<212> PRT
<213> artificial sequence

10 <400> 12
Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu
1 5 10 13

Sequence Listing

<110> Lee, James
Wood, William I.

<120> VEGF-RELATED PROTEIN

<130> P0963R1D1

<140> US 09/313,299

<141> 1999-05-17

<150> US 08/706,054

<151> 1996-08-30

<150> US 60/003,491

<151> 1995-09-08

<160> 12

<210> 1

<211> 2031

<212> DNA

<213> Human

<220>

<221> Human

<222> 1-2031

<223> Sequence source: VRP

<400> 1

cgcggggtgt tctggtgtcc cccgccccgc ctctccaaaa agctacaccg 50
acgcggaccg cggcggcgctc ctccctcgcc ctgcgttcac ctgcggggct 100
ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggc ttttacctga 150
caccgcgcgc ctttccccgg cactggctgg gagggcgccc tgcaaagttg 200
ggaacgcgga gccccggacc cgctcccgcc gcctccggct cgcccagggg 250
gggtcgccgg gaggagcccc ggggagaggg accaggaggg gcccgcggcc 300
tcgcaggggc gcccgcgccc ccacccctgc ccccgccagc ggaccgggtcc 350
cccacccccg gtccctccac catgcacttg ctgggcttct tctctgtggc 400
gtgttctctg ctgcgcgctg cgctgctccc gggctctgc gaggcgcccc 450
ccgcgcgcgc cgccttcgag tccggactcg acctctcgga cgcggagccc 500
gacgcgggcg aggccacggc ttatgcaagc aaagatctgg aggagcagtt 550
acggtctgtg tccagtgtag atgaactcat gactgtactc taccagaat 600
attggaaaat gtacaagtgt cagctaagga aaggaggctg gcaacataac 650
agagaacagg ccaacctcaa ctcaaggaca gaagagacta taaaatttgc 700
tgcagcacat tataatacag agatcttgaa aagtattgat aatgagtgga 750
gaaagactca atgcatgcca cgggaggtgt gtatagatgt ggggaaggag 800

tttggagtcg cgacaaacac cttcttttaa cctccatgtg tgtccgtcta 850
 cagatgtggg gggttgctgca atagtgaggg gctgcagtg atgaacacca 900
 gcacgagcta cctcagcaag acgttatattg aaattacagt gcctctctct 950
 caaggcccca aaccagtaac aatcagtttt gccaatcaca cttcctgccg 1000
 atgcatgtct aaactggatg ttacagaca agttcattcc attattagac 1050
 gttccctgcc agcaacacta ccacagtgtc aggcagcgaa caagacctgc 1100
 cccaccaatt acatgtggaa taatcacatc tgcagatgcc tggctcagga 1150
 agattttatg ttttctcgg atgctggaga tgactcaaca gatggattcc 1200
 atgacatctg tggaccaaac aaggagctgg atgaagagac ctgtcagtgt 1250
 gtctgcagag cggggcttcg gcctgccagc tgtggacccc acaaagaact 1300
 agacagaaac tcatgccagt gtgtctgtaa aaacaaactc tccccagcc 1350
 aatgtggggc caaccgagaa tttgatgaaa acacatgcca gtgtgtatgt 1400
 aaaagaacct gcccagaaa tcaacccta aatcctggaa aatgtgcctg 1450
 tgaatgtaca gaaagtccac agaaatgctt gttaaaagga aagaagttcc 1500
 accaccaaac atgcagctgt tacagacggc catgtacgaa ccgccagaag 1550
 gcttgtgagc caggattttc atatagtga gaagtgtgtc gttgtgtccc 1600
 ttcataattg aaaagaccac aaatgagcta agattgtact gttttccagt 1650
 tcatcgattt tctattatgg aaaactgtgt tgccacagta gaactgtctg 1700
 tgaacagaga gacccttgtg ggtccatgct aacaaagaca aaagtctgtc 1750
 tttcctgaac catgtggata actttacaga aatggactgg agctcatctg 1800
 caaaaggcct cttgtaaaga ctggttttct gccaatgacc aaacagccaa 1850
 gattttcttc ttgtgatttc tttaaaagaa tgactatata atttatttcc 1900
 actaaaaata ttgtttctgc attcattttt atagcaacaa caattggtaa 1950
 aactcactgt gatcaatatt tttatatcat gcaaaatatg tttaaaataa 2000
 aatgaaaatt gtattaaaaa aaaaaaaaaa a 2031

<210> 2
 <211> 2031
 <212> DNA
 <213> Human

<220>
 <221> Human
 <222> 1-2031
 <223> Sequence source: complement to SEQ ID NO. 1
 <400> 2

Page 286

87

tttttttttt ttttttaata caattttcat tttatttttaa acatatttttg 50
 catgatataa aaatattgat cacagtgagt tttaccaatt gttgttgcta 100
 taaaaatgaa tgcagaaaca atatttttag tggaaataaa ttatatagtc 150
 attcttttaa agaaatcaca agaggaaaat cttggctggt tggtcattgg 200
 cagaaaacca gtcttttaca gaggcctttt gcagatgagc tccagtccat 250
 ttctgtaaag ttatccacat ggttcaggaa agacagactt ttgtctttgt 300
 tagcatggac ccacaagggg ctctctgttc acagacagtt ctactgtggc 350
 aacacagttt tccataatag aaaatcgatg aactggaaaa cagtacaatc 400
 ttagctcatt tgtggtcttt tccaatatga agggacacaa cgacacactt 450
 cttcactata tgaaaatcct ggctcacaag ccttctggcg gttcgtacat 500
 ggccgtctgt aacagctgca tgtttggtgg tggaaacttct ttccttttaa 550
 caagcatttc tgtggacttt ctgtacattc acaggcacat tttccaggat 600
 ttaggggttg atttctgggg caggttcttt tacatacaca ctggcatgtg 650
 ttttcatcaa attctcggtt ggccccacat tggctgggga agagtttgtt 700
 tttacagaca cactggcatg agtttctgtc tagttctttg tgggggtccac 750
 agctggcagg ccgaagcccc gctctgcaga cacactgaca ggtctcttca 800
 tccagctcct tgtttggtcc acagatgtca tggaaatccat ctgttgagtc 850
 atctccagca tccgaggaaa acataaaatc ttctgagcc aggcattctgc 900
 agatgtgatt attccacatg taattggtgg ggcaggctctt gttcgtctgcc 950
 tgacactgtg gtagtggtgc tggcaggga cgtctaataa tggaatgaac 1000
 ttgtctgtaa acatccagtt tagacatgca tcggcaggaa gtgtgattgg 1050
 caaaactgat tgttactggt ttggggcctt gagagagagg cactgtaatt 1100
 tcaaataacg tcttgctgag gtagctcgtg ctggtgttca tgcactgcag 1150
 cccctcacta ttgcagcaac ccccatctt gtagacggac acacatggag 1200
 gtttaaagaa ggtggttgtc gcgactccaa actccttccc cacatctata 1250
 cacacctccc gtggcatgca ttgagtcttt ctccactcat tatcaatact 1300
 tttcaagatc tctgtattat aatgtgctgc agcaaatttt atagtctctt 1350
 ctgtccttga gttgaggttg gcctgttctc tgttatgttg ccagcctcct 1400
 ttccttagct gacacttgta cattttccaa tattctgggt agagtacagt 1450
 catgagttca tctacactgg acacagaccg taactgctcc tccagatctt 1500
 tgcttgcata agccgtggcc tcgcccgcgt cgggctccgc gtccgagagg 1550

tcgagtcgag actcgaaggc ggcggcgggc ggcggcgccct cgcgaggacc 1600
 cgggagcagc acagcggcga gcagagaaca cgccacagag aagaagccca 1650
 gcaagtgcac ggtggaagga ccgggggtgg gggaccggtc cgctggcggg 1700
 ggcaggggtg ggggcgcggg cgccctgcg aggcgcggg cccctcctgg 1750
 tccctctccc ccgggctcct ccgggcgacc cccctggggc gagccggagg 1800
 cggcgggagc ggggtccgggg ctccgcgttc ccaactttgc agggcgccct 1850
 ccagccagt accggggaaa ggcggcgggt gtcaggtaaa agcctcacag 1900
 gaaaccggac atccgagctc cccgcattcg gagcccgca ggtgaagcga 1950
 gggcgaggga ggacgccgcc gcggtccgcg tcggtgtagc tttttggaga 2000
 ggcggggcgg gggacaccag aacaccccg c 2031

<210> 3
 <211> 419
 <212> PRT
 <213> Human

<220>
 <221> Human
 <222> 1-419
 <223> Sequence source: VRP

<400> 3
 Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala
 1 5 10 15
 Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala
 20 25 30
 Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
 35 40 45
 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu
 50 55 60
 Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
 65 70 75
 Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
 80 85 90
 Gln His Asn Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu
 95 100 105
 Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
 110 115 120
 Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
 125 130 135
 Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
 140 145 150
 Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys

	155		160		165
Cys Asn Ser Glu Gly	Leu Gln Cys Met	Asn Thr Ser Thr Ser Tyr			
	170		175		180
Leu Ser Lys Thr Leu	Phe Glu Ile Thr	Val Pro Leu Ser Gln Gly			
	185		190		195
Pro Lys Pro Val Thr	Ile Ser Phe Ala	Asn His Thr Ser Cys Arg			
	200		205		210
Cys Met Ser Lys Leu	Asp Val Tyr Arg	Gln Val His Ser Ile Ile			
	215		220		225
Arg Arg Ser Leu Pro	Ala Thr Leu Pro	Gln Cys Gln Ala Ala Asn			
	230		235		240
Lys Thr Cys Pro Thr	Asn Tyr Met Trp	Asn Asn His Ile Cys Arg			
	245		250		255
Cys Leu Ala Gln Glu	Asp Phe Met Phe	Ser Ser Asp Ala Gly Asp			
	260		265		270
Asp Ser Thr Asp Gly	Phe His Asp Ile	Cys Gly Pro Asn Lys Glu			
	275		280		285
Leu Asp Glu Glu Thr	Cys Gln Cys Val	Cys Arg Ala Gly Leu Arg			
	290		295		300
Pro Ala Ser Cys Gly	Pro His Lys Glu	Leu Asp Arg Asn Ser Cys			
	305		310		315
Gln Cys Val Cys Lys	Asn Lys Leu Phe	Pro Ser Gln Cys Gly Ala			
	320		325		330
Asn Arg Glu Phe Asp	Glu Asn Thr Cys	Gln Cys Val Cys Lys Arg			
	335		340		345
Thr Cys Pro Arg Asn	Gln Pro Leu Asn	Pro Gly Lys Cys Ala Cys			
	350		355		360
Glu Cys Thr Glu Ser	Pro Gln Lys Cys	Leu Leu Lys Gly Lys Lys			
	365		370		375
Phe His His Gln Thr	Cys Ser Cys Tyr	Arg Arg Pro Cys Thr Asn			
	380		385		390
Arg Gln Lys Ala Cys	Glu Pro Gly Phe	Ser Tyr Ser Glu Glu Val			
	395		400		405
Cys Arg Cys Val Pro	Ser Tyr Trp Lys	Arg Pro Gln Met Ser			
	410		415		419

<210> 4
 <211> 147
 <212> PRT
 <213> Human

<220>
 <221> Human
 <222> 1-147
 <223> Sequence source: VEGE-121

<400> 4

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	
1				5					10					15	
Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	
				20					25					30	
Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	
				35					40					45	
Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	
				50					55					60	
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	
				65					70					75	
Ser	Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	
				80					85					90	
Gly	Leu	Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	
				95					100					105	
Ile	Met	Arg	Ile	Lys	Pro	His	Gln	Gly	Gln	His	Ile	Gly	Glu	Met	
				110					115					120	
Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp	
				125					130					135	
Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys	Pro	Arg	Arg				
				140					145		147				

<210> 5

<211> 149

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-149

<223> Sequence source: PIGE-131

<400> 5

Met	Pro	Val	Met	Arg	Leu	Phe	Pro	Cys	Phe	Leu	Gln	Leu	Leu	Ala	
1				5					10					15	
Gly	Leu	Ala	Leu	Pro	Ala	Val	Pro	Pro	Gln	Gln	Trp	Ala	Leu	Ser	
				20					25					30	
Ala	Gly	Asn	Gly	Ser	Ser	Glu	Val	Glu	Val	Val	Pro	Phe	Gln	Glu	
				35					40					45	
Val	Trp	Gly	Arg	Ser	Tyr	Cys	Arg	Ala	Leu	Glu	Arg	Leu	Val	Asp	
				50					55					60	
Val	Val	Ser	Glu	Tyr	Pro	Ser	Glu	Val	Glu	His	Met	Phe	Ser	Pro	
				65					70					75	
Ser	Cys	Val	Ser	Leu	Leu	Arg	Cys	Thr	Gly	Cys	Cys	Gly	Asp	Glu	
				80					85					90	
Asn	Leu	His	Cys	Val	Pro	Val	Glu	Thr	Ala	Asn	Val	Thr	Met	Gln	

	95	100	105
Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu			
	110	115	120
Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu			
	125	130	135
Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg			
	140	145	149

<210> 6
 <211> 299
 <212> DNA
 <213> Unknown

<220>
 <223> Sequence source: EST

<220>
 <221> unsure
 <222> 74
 <223> unknown base

<400> 6
 ccgtctacag atgtgggggt tgctgcaata gtgaggggct gcagtgcattg 50
 aacaccagca cgagctacct cagnaagacg ttatttgaaa ttacagtgcc 100
 tctctctcaa ggccccaac cagtaacaat cagttttgcc aatcacactt 150
 cctgccgatg catgtctaaa ctggatgttt acagacaagt tcattccatt 200
 attagacgtt ccctgccagc aacactacca cagtgtcagg cagcgaacaa 250
 gacctgcccc accaattaca tgtggaataa tcacatctgc agatgcctg 299

<210> 7
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence source: synthetic probe

<400> 7
 ctggtgttca tgcactgcag ccoctcacta ttgcagcaac ccccatctt 50

<210> 8
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence source: synthetic probe

<400> 8
 gcatctgcag atgtgattat tccacatgta attggtgggg caggtcttgt 50

<210> 9
 <211> 8
 <212> PRT

<213> Human

<220>

<221> Human

<222> 1-8

<223> Sequence source: Flt4 partial sequence

<400> 9

Tyr Ser Met Thr Pro Pro Thr Leu
1 5 8

<210> 10

<211> 9

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-9

<223> Sequence source: Flt4 partial sequence

<400> 10

Ser Leu Arg Arg Arg Gln Gln Gln Asp
1 5 9

<210> 11

<211> 40

<212> PRT

<213> Unknown

<220>

<223> Sequence source: Herpes glycoprotein D partial sequence

<400> 11

Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn
1 5 10 15

Arg Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln Leu Leu Glu
20 25 30

Gly Gly Ala Ala His Tyr Ala Leu Leu Pro
35 40

<210> 12

<211> 13

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-13

<223> Sequence source: partial VRP sequence

<400> 12

Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu
1 5 10 13



45
100

Application No.: _____

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: *Diskette submitted was blank.*

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE